CRISPR Cas9 (RNP) Editing Experiment Template

Structured Documentation for Genome Editing — From sgRNA Design and RNP Electroporation Through T7E1 and ICE-Sanger Editing Verification

Applies to

- Academic and molecular-biology research laboratories
- Biotechnology and pharmaceutical R&D groups
- Genome-editing and cell-engineering teams
- Contract research organizations (CROs)

Relevant compliance & integrity frameworks

- **FDA 21 CFR Part 11** — Electronic records and signatures
- **Institutional Biosafety (IBC)** — NIH Guidelines for research with recombinant nucleic acids
- **Data integrity (ALCOA+)** — Attributable, contemporaneous, defensible records
- **NIH / NSF** — Reproducibility and data-management requirements

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1. Executive Summary

In genome editing, the editing efficiency is a decision number. The percentage of alleles carrying an indel — and the spectrum of indels behind it — is what tells a project whether a knockout worked, which guide to carry forward, and whether an edited population is clean enough to clone. But an editing number is only as trustworthy as the guide design, the delivery, and the verification behind it. An efficiency read from a single T7E1 gel with no sequence-level confirmation is not a weak result — it is an ambiguous one. A guide chosen without off-target scoring can cut in the wrong place entirely. And when guide sequences, electroporation settings, gel images, and Sanger traces live scattered across design tools, instruments, and shared drives, editing outcomes cannot be compared reliably across guides and cell lines — which is the entire point of an editing campaign.

The ELabELN CRISPR Cas9 (RNP) Editing Experiment Template solves this by providing a pre-built, fully structured edit record that loads from the template library in a single click. It ships with a 10-step RNP electroporation protocol, validated sgRNA-design references, pre-wired editing-verification fields, and typed inputs for target gene, sgRNA sequence and name, PAM, cell line, delivery method, Cas9 source, electroporation program, editing efficiency, T7E1 cleavage, ICE indel score, and clone genotype. The Cas9 protein, synthetic sgRNA, electroporation reagents, and PCR primers link to the ELabELN inventory, and the tamper-evident audit trail captures every guide-design choice, every electroporation, and every editing-efficiency call.

This white paper describes what the template contains, the genome-editing use case it is designed to support, the upstream and downstream workflows it connects to, the benefits it delivers to the scientist, and how a laboratory can deploy it and begin running edits within days.

> **Key benefit**
> Labs that adopt the CRISPR template stop rebuilding the editing workflow every time and lose no guide sequence, electroporation setting, or indel call between the design tool, the instrument, and the notebook. Editing is gated by sequence-level verification, every efficiency carries its guide and indel spectrum, and outcomes become queryable across guides and cell lines — the structured, comparable foundation a real editing campaign and defensible, biosafety-reviewable provenance depend on.

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2. What Is CRISPR-Cas9 Editing, and Why Does Documentation Matter?

2.1 The Technique

CRISPR-Cas9 editing uses a single guide RNA (sgRNA) to direct the Cas9 nuclease to a specific genomic site, where it creates a double-strand break next to a PAM sequence. The cell repairs the break, most often by non-homologous end joining, which introduces small insertions or deletions (indels) that disrupt the target — the basis of a gene knockout. Delivering Cas9 and the sgRNA as a pre-complexed ribonucleoprotein (RNP) by electroporation gives fast, transient, high-efficiency editing without a plasmid. A few days later the edited population is genotyped: a T7E1 mismatch assay gives a quick gel-based estimate of editing, and PCR-Sanger sequencing across the cut site — deconvolved with a tool such as ICE — gives the sequence-level editing efficiency and the full indel spectrum.

An editing number is only meaningful if the whole chain performed: a well-scored, on-target guide, an efficient RNP delivery, cells that recovered, and a verification method that resolves the actual edits rather than merely suggesting them. Weakness anywhere in that chain produces an efficiency that looks convincing and is not — an off-target guide, a mis-estimating gel, or a population too mixed to interpret.

Because editing efficiency and the indel spectrum decide which guide advances and which clones are worth isolating, and are compared across guides and cell lines, **the guide sequence, the delivery conditions, the T7E1 result, and the ICE indel spectrum are what make an edit trustworthy and comparable to the next one — which is exactly why they must live in one structured, queryable record rather than a folder of gel images and Sanger traces.**

2.2 The Documentation Problem

Recording edits across design tools, instruments, gel images, and paper notebooks creates a set of interconnected risks:

- The guide sequence, PAM, and off-target scoring are recorded inconsistently, so a guide's design rationale is lost and its choice cannot be defended later.
- Electroporation program and RNP conditions are rebuilt from memory each time, so an inconsistent delivery quietly makes efficiencies non-comparable across guides.
- The T7E1 gel image is saved to a shared drive, and the editing estimate is remembered rather than recorded against the edit.
- The Sanger trace and ICE indel spectrum sit in separate files, unlinked to the guide, cell line, and electroporation that produced them.
- Editing efficiency and indel outcomes are noted in free text, so cross-guide comparison cannot be queried.
- Cas9, sgRNA, and reagent lots are not captured against the edit, so a shift in efficiency cannot be traced to a reagent batch.
- Biosafety (IBC) approval is filed elsewhere, so the edit record does not carry the containment context regulators and committees expect.

These are the gaps that make editing data hard to trust and compare, and they are the gaps this template was designed to close.

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3. Template Overview: What Ships with the Template

The ELabELN CRISPR Cas9 (RNP) Editing Experiment Template is a pre-populated experiment record available to all ELabELN subscribers directly from the template library. It ships configured for targeted editing of the BCL11A erythroid enhancer in HEK293T cells using Cas9 ribonucleoprotein electroporation, with a 10-step protocol covering sgRNA design through ICE-Sanger verification of editing efficiency. The default protocol assumes a Lonza 4D-Nucleofector with the SF cell-line kit, 5 µg recombinant SpCas9 pre-complexed with 100 pmol synthetic sgRNA at room temperature, 200,000 HEK293T cells per nucleofection, T7E1 mismatch detection 72 hours post-edit, and PCR-Sanger sequencing of the locus with ICE (Synthego) deconvolution. Every section is editable — the configuration is a tested baseline, not a locked format.

3.1 Template Sections at a Glance

The template populates the existing ELabELN experiment sections your lab already works in. Your team edits a working baseline instead of rebuilding the editing workflow from scratch every time.

Section	What it pre-populates
Main Text	The edit objective, the sgRNA design rationale and off-target risk notes, and the expected editing efficiency, authored in the TinyMCE rich-text editor and linked to the cell line and biosafety record.
Extra Fields	Twelve structured, typed fields grouped as Target, Guide & Delivery, and Verification — target gene, sgRNA sequence, sgRNA name, PAM, cell line, delivery method, Cas9 source, electroporation program, editing efficiency, T7E1 cleavage, ICE indel score, and clone genotype. Typed values make editing outcomes queryable across guides.
Steps	A 10-step workflow checklist covering sgRNA design through ICE verification. Each tick is timestamped to the audit trail, and the nucleofection run is auto-logged.
Compounds	The recombinant Cas9, synthetic sgRNA, SF nucleofection reagents, T7E1 enzyme, and PCR primers pre-linked from the compound database, with lot numbers carried in automatically and the guide sequence shown inline.
Links & Resources	Pre-wired to the lab's CRISPR RNP SOP v2.0, the CRISPick sgRNA design-tool output, and the IBC (Institutional Biosafety Committee) approval record.
Storage & Files	−80 °C Cas9 and sgRNA stock storage, plus labelled attachment slots for T7E1 gel images and ICE Sanger traces (AB1 and PNG).

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Main Text
Edit objective, sgRNA design rationale, expected editing efficiency (TinyMCE).
Extra Fields
Typed: target, sgRNA, PAM, cell line, Cas9 source, electroporation, efficiency.
Steps
10-step checklist; each tick timestamped, nucleofection run logged.
Compounds
Recombinant Cas9, synthetic sgRNA, SF reagents, T7E1 enzyme, PCR primers.
Links & Resources
CRISPR RNP SOP v2.0, CRISPick design output, IBC approval linked.
Storage & Files
−80 °C Cas9 & sgRNA storage; T7E1 gels + ICE Sanger traces (AB1 + PNG).

Figure 1. The six ELabELN experiment sections pre-populated by the CRISPR Cas9 (RNP) editing template.

3.2 The 10-Step Protocol

The workflow checklist is the operational spine of the template. Each step maps to a discrete bench or analysis action and writes a timestamped, user-attributed entry to the audit trail when checked off. The nucleofection run is auto-logged, and the Sanger sequencing and ICE deconvolution are performed with external tools, with the resulting values recorded as typed fields.

Step	Action	What it captures
1	Design sgRNA	Target gene; sgRNA sequence; PAM; off-target score
2	Order & QC guide	Synthetic sgRNA; guide QC
3	Complex Cas9 RNP	Cas9 source; RNP ratio
4	Nucleofect cells	Cell line; delivery; electroporation program
5	Recover (culture)	Recovery conditions
6	Extract gDNA (72 h)	Genomic DNA for genotyping
7	PCR amplicon	Locus amplicon; primers
8	T7E1 screen	T7E1 cleavage (gel estimate)
9	Sanger sequence	Sanger trace of the locus (external)
10	ICE indel score	Editing efficiency; indel spectrum (external); e-signature

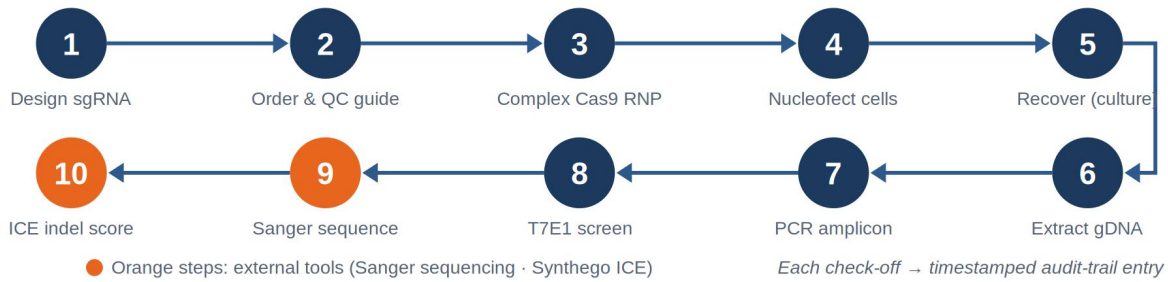

Figure 2. The 10-step CRISPR RNP editing workflow — orange steps use external tools (Sanger sequencing and Synthego ICE deconvolution); every check-off writes a timestamped entry to the ELabELN audit trail.

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4. The Use Case: When and How the Template Is Used

The template is intended as a tested baseline for academic, biotechnology, and pharmaceutical labs running genome editing. It is configured around a recognizable reference — a BCL11A enhancer knockout in HEK293T cells — but the scenarios it serves span the editing bench and the cell-engineering campaign it feeds.

4.1 Gene Knockout and Editing Efficiency (Primary Use Case)

The core scenario: disrupting a target and measuring how efficiently it was edited. The template captures the guide, the delivery, the T7E1 screen, and the ICE indel spectrum in one structured record, so an editing result is fully reconstructable — which guide, which cell line, which delivery, which indels — rather than a percentage in a notebook detached from the run that produced it.

4.2 Guide Design and Screening

Choosing a guide means comparing candidates on predicted on-target activity, off-target risk, and measured editing. Because each guide's design and efficiency are structured and queryable, the best guide is chosen from the records rather than reconstructed from scattered design-tool exports, and each choice is linked to the scoring and result that justify it.

4.3 Knock-In, Base Editing, and Prime Editing

Beyond knockouts, the same record structures precise edits. Because the target, guide, Cas9 variant, and verification are typed fields, the template extends to HDR knock-ins, base editing, and prime editing by editing the guide and analysis sections — the outcome and its verification captured the same way.

4.4 Multiplex and Library Screening

Editing scales from a single guide to many. Because the record structures the guide and its outcome, it extends to multiplex edits and pooled library screens, with each guide's design and editing result tracked in a comparable form for downstream hit analysis.

4.5 Editing-Efficiency and Off-Target QC Across Guides

Because editing efficiency, indel score, and guide design are typed and queryable, the template doubles as a running editing-QC record. A team can pull every guide against a target, compare efficiencies and indel spectra side by side, and flag a guide whose off-target profile or low efficiency rules it out — before it is carried into a cell line.

4.6 Multi-Site and CRO Collaboration

Editing work is often shared across labs, cores, and partners. Because every ELabELN edition includes unlimited users, the PI, scientists, and collaborators can all work from the same records. Granular permissions let project leads control who can edit CRISPR runs versus only review them — important during the multi-site collaborations that editing and screening campaigns frequently involve.

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5. Dependencies and Connected Workflows

The CRISPR template does not exist in isolation. It sits inside a network of connected workflows — upstream, parallel, external, and downstream — that give the edit record its full scientific and decision-making value.

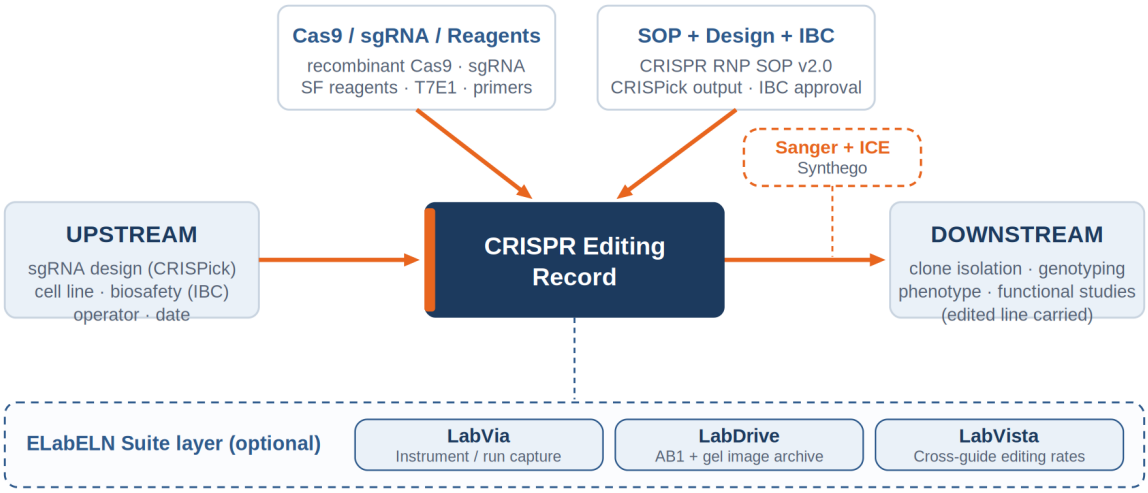

Figure 3. The template connects an upstream guide-design and biosafety-approval workflow, parallel inventory and SOP/design/IBC systems, the external Sanger and ICE analysis tools, and downstream clone-isolation, genotyping, and functional-study workflows.

5.1 Upstream: Guide Design, Cell Line, and Biosafety

Every edit begins with a designed guide, a chosen cell line, and biosafety approval to proceed. The template links to the upstream sgRNA design (for example, CRISPick output), the cell line, and the IBC approval, so opening an edit surfaces the guide and its rationale, the operator, and the date — connecting each editing result to the design and authorization behind it.

5.2 Parallel: Cas9, sgRNA, and Reagent Inventory

The Compounds section links the recombinant Cas9, synthetic sgRNA, SF nucleofection reagents, T7E1 enzyme, and PCR primers directly to the ELabELN inventory. Because reagent identity bears on editing efficiency, this traceability is decisive. Through the link the record automatically carries:

- **Lot numbers and aliquot tracking** for the Cas9, guide, and reagents, so a shift in efficiency can be traced to a reagent batch.
- **The guide sequence, shown inline**, so the exact guide and PAM are on the record and reproducible.
- **Expiry and stock levels**, with low-stock warnings before a run, so an edit is not started against a depleted or expired reagent.

Barcode and QR scanning can populate these links from the physical vial, keeping lot capture effortless across an editing experiment.

5.3 Parallel: SOPs, the Design Output, and Biosafety Approval

The Links section connects the edit to the lab's CRISPR RNP SOP, the sgRNA design-tool output, and the IBC approval record. That biosafety link is what makes the edit defensible: each

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edit opens alongside the SOP it followed and the approval that authorized it, so the containment context is built in rather than filed separately.

5.4 External: Sanger Sequencing and ICE Deconvolution

The sequence-level verification runs outside ELabELN: PCR products are Sanger-sequenced, and the traces are deconvolved with a tool such as Synthego ICE to yield the editing efficiency and indel spectrum. ELabELN is the system of record around those tools: the indel spectrum (insertion and deletion sizes and frequencies) lives in the spreadsheet editor, the Sanger AB1 traces and T7E1 gel images attach in the Storage & Files section, and the editing efficiency and ICE indel score are written back into the typed Verification fields. The evidence and the reported efficiency stay together in one record.

5.5 Downstream: Clone Isolation, Genotyping, and Function

The edited population feeds clone isolation and single-cell genotyping, phenotypic and functional studies, and further engineering — and, because editing efficiency and indel outcomes are typed and queryable, cross-guide and cross-line comparison. A decision to clone or to re-design a guide rests on a documented, comparable editing result rather than a number recalled from memory.

5.6 The ELabELN Suite: Instruments and Dashboards

Everything above is available in ELabELN Standard. Labs on the ELabELN Suite gain three layers that connect to the same record: LabVia captures data directly from the nucleofector and other instruments; LabDrive adds metadata search, versioning, and role-based access across Sanger-trace and gel-image archives; and LabVista builds cross-guide editing-efficiency dashboards on the structured editing metadata. The same audit trail and data-integrity controls span all layers.

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6. How the Scientist Benefits

The template is built to deliver value at the bench and to the campaign alike. The benefits compound with every edit a lab runs.

6.1 Start From a Tested Baseline, Not a Blank Workflow

The scaffold — protocol, typed fields, guide and reagent links, SOP, design output, and biosafety link — is already built. The scientist edits a working configuration to match the target and cell line they actually edit, rather than rebuilding the workflow from scratch every time. The first edit is faster, and every subsequent one is consistent and comparable.

6.2 Document by Doing

Checking off each of the 10 steps as it happens produces a contemporaneous, timestamped record as a by-product of the edit, and the nucleofection run is auto-logged. There is no separate write-up to reconstruct later.

6.3 Never Lose Guide or Indel Provenance Again

Because the guide is a structured field and the reagents are linked to inventory, the guide sequence, delivery conditions, lots, and indel spectrum are captured permanently on every edit. When an editing result is questioned, the guide and its provenance are on the record — closing the most common editing troubleshooting gap by default.

6.4 Cross-Guide Editing Efficiency You Can Query

Typed editing-efficiency, indel-score, and guide fields make the campaign queryable. A team can pull every guide against a target, trend efficiency guide by guide, and gate on sequence-level verification at a glance — turning a folder of gel images and Sanger traces into a live editing view.

6.5 Verification Gating and Biosafety-Reviewable Provenance

Capturing the ICE indel spectrum beside every efficiency makes sequence-level verification a visible, queryable gate rather than an afterthought, and the tamper-evident audit trail, reagent traceability, IBC-approval link, and electronic signatures give each edit a defensible provenance — structured to support biosafety-committee review and FDA 21 CFR Part 11 review when the lab's quality system requires it.

> **At the bench, in practice**
>
> A scientist opens the template, sets the target and guide to match today's edit, scans the Cas9 and reagent vials to capture their lots, and checks off each step as the RNP is complexed, the cells are nucleofected and recovered, and the locus is amplified. The T7E1 gel gives a first read; the Sanger trace is deconvolved in ICE, and the editing efficiency and indel spectrum go into typed fields — the sequence-level result confirming the edit was real. Weeks later, comparing guides, the project lead queries every guide against the target and watches editing efficiency trend, guide by verified guide.

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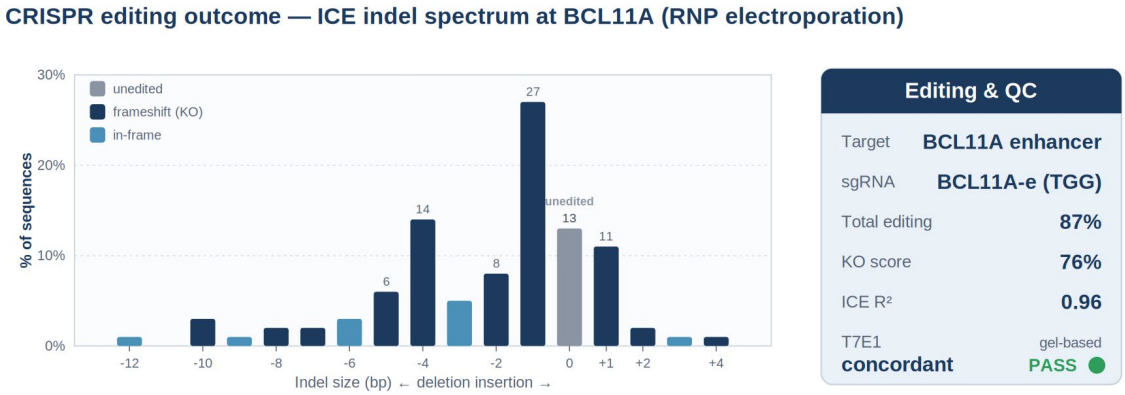
7. The Indel Spectrum and Editing Quality

7.1 The Default Reference: A BCL11A Enhancer Knockout

The template ships configured for a Cas9 RNP edit of the BCL11A erythroid enhancer in HEK293T cells: a designed sgRNA pre-complexed with recombinant SpCas9, delivered by 4D-Nucleofector electroporation into 200,000 cells, recovered in culture, and genotyped 72 hours later. A T7E1 mismatch assay gives a quick gel-based read, and PCR-Sanger sequencing across the cut site is deconvolved with ICE to return the editing efficiency and the full indel spectrum — with in-frame and frameshift outcomes distinguished so the knockout score is legible at a glance. This concrete reference demonstrates the full design-to-verification workflow out of the box; swap the target, guide, cell line, or Cas9 variant to match what your lab edits.



Illustrative — the indel spectrum, Sanger traces and gel images are captured in ELabELN; editing efficiency and ICE indel score are recorded as typed fields.

Figure 4. A CRISPR editing-outcome indel spectrum from ICE deconvolution — indel size against percent of sequences, colored by unedited, frameshift (knockout), and in-frame — alongside the editing-and-QC panel (with T7E1 concordance). Illustrative; the indel spectrum and traces are captured in ELabELN, and editing efficiency and ICE indel score are recorded as typed fields.

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7.2 How the Template Handles the Guide, Verification, and Indel Spectrum

The full indel spectrum — insertion and deletion sizes and their frequencies — lives in the spreadsheet editor, structured for direct cross-guide comparison. The T7E1 gel image and the Sanger AB1 traces attach in the Storage & Files section, and the editing efficiency, T7E1 cleavage, and ICE indel score are written back into the typed Verification fields. Because these values are structured and queryable, cross-guide comparison is straightforward: query every guide against a target, gate on sequence-level verification, and review editing efficiency and indel spectrum side by side — the editing view a campaign runs on. Verification can be configured to use T7E1, ICE-Sanger, amplicon-NGS, ddPCR, or flow-based reporter assays depending on the lab's preferred workflow.

Element	Default configuration	Editable to
Target gene / locus	BCL11A erythroid enhancer	Any gene, enhancer, or locus
sgRNA / design	Synthetic sgRNA (CRISPick)	Benchling, CHOPCHOP, IDT; multiplex / library
Cell line	HEK293T	K562, U2OS, primary T cells, iPSCs
Delivery	RNP electroporation (4D-Nucleofector)	Lipofection, viral transduction
Cas9 variant	WT SpCas9	HiFi, dCas9-VPR, base editor, prime editor
Verification	T7E1 + ICE-Sanger	Amplicon-NGS, ddPCR, flow reporter

Figure 5. The template's default configuration — fully editable for any target, guide, cell line, delivery method, Cas9 variant, or verification method.

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8. Configuring the Template for Your Edit

Adapting the template to a different target or editing strategy is a matter of editing the relevant sections — not rebuilding the structure.

8.1 Swap the Target and Guide

Change the target gene and sgRNA sequence — designed in Benchling, CRISPick, CHOPCHOP, or IDT — by editing the Target and Guide sections. Record the PAM and off-target scoring alongside the sequence so the guide choice stays defensible.

8.2 Change the Cell Line and Delivery

Switch the cell line (HEK293T, K562, U2OS, primary T cells, iPSCs) and the delivery method (electroporation, lipofection, viral transduction) by editing the Guide & Delivery section. The verification and indel-spectrum fields apply regardless of how the editor reaches the cell.

8.3 Change the Cas9 Variant and Verification

Move from wild-type SpCas9 to a HiFi variant, dCas9-VPR, a base editor, or a prime editor, and configure verification to use T7E1, ICE-Sanger, amplicon-NGS, ddPCR, or a flow-based reporter, by editing the Verification section. Single-guide edits extend to multiplex and library screening the same way.

8.4 Save a Custom Version

Once configured, save your edits as a private template scoped to your lab, or publish back to the ELabELN template library. Every subsequent edit opens from your configured baseline, and separate versions can be maintained for different targets, cell lines, or editing strategies.

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9. Getting Started

ELabELN Standard is a cloud-hosted SaaS deployment typically live within one to two business days of account creation. There is no hardware to buy, no IT project, and no per-seat licensing.

1. **Start an ELabELN account.** Visit elabeln.com/get-started. ELabELN Standard runs on LabLynx's managed cloud infrastructure.
2. **Provision your instance.** LabLynx provisions the instance within one to two business days; you receive a URL, admin credentials, and onboarding documentation.
3. **Load the CRISPR template.** From the template library, select the CRISPR Cas9 (RNP) editing template and click "Use This Template." An editable instance opens immediately.
4. **Add your Cas9, guides, and reagents to the inventory.** Enter your recombinant Cas9, synthetic sgRNAs, nucleofection reagents, T7E1 enzyme, and PCR primers with lot numbers and −80 °C storage locations. This is a one-time setup step.
5. **Link your SOP, design output, and IBC approval.** Upload your CRISPR RNP SOP and sgRNA design-tool output, and connect your Institutional Biosafety Committee approval to the template's Links section.
6. **Customize the template for your edit.** Edit the target, guide, cell line, delivery method, and Cas9 variant, then save as a private team version.
7. **Run your first edit.** Open your saved template, complete the 10-step checklist, capture the guide and delivery, record the T7E1 and ICE editing efficiency, attach the Sanger trace and gel image, and sign off.

Typical timeline

Day 1: Account requested at elabeln.com/get-started. Day 2–3: Instance provisioned; Cas9, guide, and reagent inventory populated; SOP, design output, and IBC approval linked. Day 3–4: Template configured and saved as a private version for your target and cell line. Day 4–5: First edit documented in ELabELN with the guide, delivery, and editing efficiency captured and an e-signature.

9.1 ELabELN Standard vs. ELabELN Suite

Capability	Standard	Suite
CRISPR template access	Included	Included
Unlimited users	Included	Included
Audit trail and e-signatures	Included	Included
Cas9 / sgRNA / reagent inventory with lot tracking	Included	Included
SOP, design-output & IBC-approval linking	Included	Included
Indel spectrum + Sanger / gel attachments	Included	Included
LabVia instrument / nucleofector capture	—	Suite layer
LabDrive Sanger / gel archive search & versioning	—	Suite layer
LabVista cross-guide editing-efficiency dashboards	—	Suite layer

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10. Frequently Asked Questions

Can I configure the template for my target gene and cell line?

Yes. Every section is editable. Swap in different target genes and sgRNA sequences (designed in Benchling, CRISPick, CHOPCHOP, IDT), change the cell line (HEK293T, K562, U2OS, primary T cells, iPSCs), adjust the delivery method (electroporation, lipofection, viral transduction), change the Cas9 variant (WT, HiFi, dCas9-VPR, base editors, prime editors), or move from single-guide to multiplex or library screening. Save your edits as a private template scoped to your lab, or publish back to the ELabELN template library.

Does the template support multiple verification methods?

Yes. The template captures both T7E1 mismatch detection (gel-based screening) and ICE-Sanger indel deconvolution (sequence-level analysis), with optional amplicon-NGS fields. The spreadsheet editor captures the indel spectrum from any of these methods, and verification can be configured to use T7E1, ICE, amplicon-NGS, ddPCR, or flow-based reporter assays depending on your lab's preferred workflow.

How does the template handle biosafety documentation?

The template includes a typed field for IBC (Institutional Biosafety Committee) approval reference, linked from the Resources section. Combined with ELabELN's tamper-evident audit trail and electronic signatures, the resulting record supports biosafety-committee review and the CRISPR-specific containment documentation required by many institutions and regulatory bodies.

Is it included in every ELabELN plan?

Yes. Every published template in the ELabELN library is available to all subscribers in both the Standard and Suite editions, with unlimited users in either edition and no per-template fee.

Can my whole lab use this template?

Yes. Every ELabELN edition includes unlimited users, so the PI, postdocs, grad students, rotating researchers, and visiting collaborators can all use the template without per-seat charges. Granular permissions let the PI control who can edit CRISPR runs versus only review them.

How quickly can my lab start running CRISPR edits in ELabELN?

ELabELN Standard cloud deployment is typically live in one to two business days. Once the instance is provisioned, the template loads from the library in a single click, with the target, sgRNA, cell line, and delivery method editable to match the edits your lab actually runs.

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11. Conclusion

The ELabELN CRISPR Cas9 (RNP) Editing Experiment Template is not simply a digital version of a gel image or a Sanger trace. It is a structured, audit-ready, searchable record that connects to your Cas9, guide, and reagent inventory, your SOPs and design outputs, the cell line and biosafety approval the edit followed, your Sanger and ICE analysis tools, and the clone-isolation, genotyping, and functional-study workflows the edited line feeds — and, in the Suite edition, cross-guide editing-efficiency dashboards. It turns an edit into a record whose guide, verification, and editing efficiency are captured, comparable, and defensible.

For a laboratory that runs edits regularly, the benefit compounds with every campaign. Guide designs, delivery conditions, and indel spectra accumulate into one queryable editing history. Every Cas9 and reagent lot is traceable. Every edit is gated by sequence-level verification and carries its biosafety context, and every edited line carries a defensible provenance — so an editing result of uncertain validity can no longer quietly drive a decision, and the cross-guide trend that guides the campaign is built in rather than reconstructed.

The template is available to all ELabELN subscribers today. A new instance is live in one to two business days, and the first structured edit is typically documented within a week of account creation.

> **Get started**
>
> Visit elabeln.com/get-started to request your ELabELN instance, or contact LabLynx at 866.522.5969 or info@lablynx.com. Load the CRISPR Cas9 (RNP) editing template, configure it for your target and cell line, and run your next edit from a tested, audit-ready baseline.

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